

SEQUENCE LISTING

<110> Edwin L. Madison
Edgar O. Ong

<120> NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE PROTEASE 7, THE
ENCODED POLYPEPTIDES AND METHODS BASED THEREON

<130> 24745-1613

<140>
<141> Herewith

<150> 60/275,592
<151> 2001-03-13

<160> 22

<170> FastSEQ for Windows Version 4.0

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<212> DNA  
<213> Homo Sapien
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<223> Nucleotide sequence encoding MTSP1

<300>
<301> O'Brien, T.J. and Tanimoto, H.
<308> GenBank #AR081724
<309> 2000-08-31
<310> 5,972,616
<311> 1998-02-20
<312> 1999-10-26

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Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His
15          20          25

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gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac 148
 Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn
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aac gtc aag aag gtg gaa aag cat ggc ccg ggg cgc tgg gtg gtg ctg 196
Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu
45 50 55

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gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc      244
Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe
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ctg gtg tgg cat ttg cag tac cg^g gac gtg cgt gtc cag aag gtc ttc 292
 Leu Val Trp His Leu Gln Tyr Arg Asp Val Arg Val Gln Lys Val Phe

24745-1613

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aac tcc aac tcc act gag ttt gta agc ctg gcc agc aag gtg aag gac Asn Ser Asn Ser Thr Glu Phe Val Ser Leu Ala Ser Lys Val Lys Asp 110		115	120	388
gcg ctg aag ctg ctg tac agc gga gtc cca ttc ctg ggc ccc tac cac Ala Leu Lys Leu Leu Tyr Ser Gly Val Pro Phe Leu Gly Pro Tyr His 125		130	135	436
aag gag tcg gct gtg acg gcc ttc agc gag ggc agc gtc atc gcc tac Lys Glu Ser Ala Val Thr Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr 140		145	150	484
tac tgg tct gag ttc agc atc ccg cag cac ctg gtg gag gag gcc gag Tyr Trp Ser Glu Phe Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu 155		160	165	532
cgc gtc atg gcc gag gag cgc gta gtc atg ctg ccc ccg cgg gcg cgc Arg Val Met Ala Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg 175		180	185	580
tcc ctg aag tcc ttt gtg gtc acc tca gtg gtg gct ttc ccc acg gac Ser Leu Lys Ser Phe Val Val Thr Ser Val Val Ala Phe Pro Thr Asp 190		195	200	628
tcc aaa aca gta cag agg acc cag gac aac agc tgc agc ttt ggc ctg Ser Lys Thr Val Gln Arg Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu 205		210	215	676
cac gcc cgc ggt gtg gag ctg atg cgc ttc acc acg ccc ggc ttc cct His Ala Arg Gly Val Glu Leu Met Arg Phe Thr Thr Pro Gly Phe Pro 220		225	230	724
gac agc ccc tac ccc gct cat gcc cgc tgc cag tgg gcc ctg cgg ggg Asp Ser Pro Tyr Pro Ala His Ala Arg Cys Gln Trp Ala Leu Arg Gly 235		240	245	772
gac gcc gac tca gtg ctg agc ctc acc ttc cgc agc ttt gac ctt gcg Asp Ala Asp Ser Val Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala 255		260	265	820
tcc tgc gac gag cgc ggc agc gac ctg gtg acg gtg tac aac acc ctg Ser Cys Asp Glu Arg Gly Ser Asp Leu Val Thr Val Tyr Asn Thr Leu 270		275	280	868
agc ccc atg gag ccc cac gcc ctg gtg cag ttg tgt ggc acc tac cct Ser Pro Met Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro 285		290	295	916
ccc tcc tac aac ctg acc ttc cac tcc cag aac gtc ctg ctc atc Pro Ser Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile 300		305	310	964
aca ctg ata acc aac act gag cgg cggt cat ccc ggc ttt gag gcc acc Thr Leu Ile Thr Asn Thr Glu Arg Arg His Pro Gly Phe Glu Ala Thr 315		320	325	1012
			330	

24745-1613

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aac att gac tgc aca tgg aac att gag gtg ccc aac aac cag cat gtg Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val 365 370 375	1156
aag gtg agc ttc aaa ttc ttc tac ctg ctg gag ccc ggc gtg cct gcg Lys Val Ser Phe Lys Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala 380 385 390	1204
ggc acc tgc ccc aag gac tac gtg gag atc aat ggg gag aaa tac tgc Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys 395 400 405 410	1252
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gaa tac ctc tcc tac gac tcc agt gac cca tgc ccg ggg cag ttc acg Glu Tyr Ile Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr 445 450 455	1396
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gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala 475 480 485 490	1492
ggc cac cag ttc acg tgc aag aac aag ttc tgc aag ccc ctc ttc tgg Gly His Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp 495 500 505	1540
gtc tgc gac agt gtg aac gac tgc gga gac aac agc gac gag cag ggg Val Cys Asp Ser Val Asn Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly 510 515 520	1588
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24745-1613

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Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu		
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Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys		
590	595	600
gac tgt ggg ctg cgg tca ttc acg aga cag gct cgt gtt gtt ggg ggc		1876
Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly		
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acg gat gcg gat gag ggc gag tgg ccc tgg cag gta agc ctg cat gct		1924
Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala		
620	625	630
ctg ggc cag ggc cac atc tgc ggt gct tcc ctc atc tct ccc aac tgg		1972
Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp		
635	640	645
650		
ctg gtc tct gcc gca cac tgc tac atc gat gac aga gga ttc agg tac		2020
Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr		
655	660	665
tca gac ccc acg cag tgg acg gcc ttc ctg ggc ttg cac gac cag agc		2068
Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser		
670	675	680
cag cgc agc gcc cct ggg gtg cag gag cgc agg ctc aag cgc atc atc		2116
Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile		
685	690	695
tcc cac ccc ttc ttc aat gac ttc acc ttc gac tat gac atc gcg ctg		2164
Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu		
700	705	710
ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtg cgg ccc atc		2212
Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile		
715	720	725
730		
tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg		2260
Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp		
735	740	745
gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc		2308
Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile		
750	755	760
ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac		2356
Ieu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn		
765	770	775
ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtg ggc ttc ctc		2404
Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu		
780	785	790
agc ggc ggc gtg gac tcc tgc cag ggt gat tcc ggg gga ccc ctg tcc		2452
Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser		
795	800	805
810		
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24745-1613

Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly Val Val Ser Trp		
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Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu		
830	835	840
cct ctg ttt cgg gac tgg atc aaa gag aac act ggg gta ta ggggccccgggg		2599
Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val		
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35 40 45		
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly		
50 55 60		
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln		
65 70 75 80		
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile		
85 90 95		
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu		
100 105 110		
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr		
115 120 125		
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr		
130 135 140		
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser		
145 150 155 160		
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu		
165 170 175		
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val		
180 185 190		
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg		
195 200 205		
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu		
210 215 220		
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala		
225 230 235 240		
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu		
245 250 255		
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly		

	260	265	270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met	275	280	285
Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr	290	295	300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr	305	310	315
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg	325	330	335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn	340	345	350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp	355	360	365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Ser Phe Lys Phe	370	375	380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp	385	390	395
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe	405	410	415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp	420	425	430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp	435	440	445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys	450	455	460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His	465	470	475
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys	485	490	495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn	500	505	510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln	515	520	525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys	530	535	540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro	545	550	555
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn	565	570	575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp	580	585	590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser	595	600	605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly	610	615	620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile	625	630	635
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His	645	650	655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp	660	665	670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly	675	680	685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn	690	695	700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro	705	710	715
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser	725	730	735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His	740	745	750

24745-1613

Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
 755 760 765
 Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
 770 775 780
 Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
 785 790 795 800
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
 805 810 815
 Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
 820 825 830
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 835 840 845
 Ile Lys Glu Asn Thr Gly Val
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<220>
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 <223> Nucleic acid sequence of protease domain of MTSP1

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24745-1613

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24745-1613

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<213> Homo Sapien

<400> 4
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20 25 30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
35 40 45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
50 55 60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65 70 75 80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
85 90 95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100 105 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115 120 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130 135 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145 150 155 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
165 170 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
180 185 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195 200 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
210 215 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Val

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
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<210> 6

24

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<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
gtcccaaact tactataacct acaatgtacc ag 32

<210> 7
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
gtccccaaact tactataacct acaatgtacc ag 32

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
aatggccatg gcaggccagc ctcc 24

<210> 9
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
tgccattacc agcatcctct tctactcaaa g 31

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
ccatgtgtat aactcacgga caatccacac tac 33

<210> 11
<211> 10
<212> PRT
<213> Homo sapien

<400> 11
Met Pro Leu Pro Ala Ser Ser Ser Thr Gln
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1          5          10
<210> 12
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
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<210> 13
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
atagcggccg cacactacat accagtcttt gaggcaatc          39

<210> 14
<211> 11
<212> PRT
<213> Homo sapien

<400> 14
Lys Arg Ile Val Gln Gly Arg Glu Thr Ala Met
 1           5           10

<210> 15
<211> 2100
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (45) ... (1361)
<223> MTSP7: full length cDNA

<220>
<221> CDS
<222> (45) ... (1361)
<223> MTSP7: full length cDNA

<400> 15
agatcagatg gcgactgaat agaagctgcc ccagtcctgg gttc atg atg tac aca      56
                                         Met Met Tyr Thr
                                         1

cct gtt gaa ttt tca gaa gct gaa ttc tca cga gct gaa tat caa aga
Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala Glu Tyr Gln Arg
 5           10           15           20           104

aag cag caa ttt tgg gac tca gta cgg cta gct ctt ttc aca tta gca
Lys Gln Phe Trp Asp Ser Val Arg Leu Ala Leu Phe Thr Leu Ala
 25           30           35           152

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24745-1613

att gta gca atc ata gga att gca att ggt att gtt act cat ttt gtt Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val Thr His Phe Val 40 45 50	200
gtt gag gat gat aag tct ttc tat tac ctt gcc tct ttt aaa gtc aca Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser Phe Lys Val Thr 55 60 65	248
aat atc aaa tat aaa gaa aat tat ggc ata aga tct tca aga gag ttt Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser Ser Arg Glu Phe 70 75 80	296
ata gaa agg agt cat cag att gaa aga atg atg tct agg ata ttt cga Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser Arg Ile Phe Arg 85 90 95 100	344
cat tct tct gta ggc ggt cga ttt atc aaa tct cat gtt atc aaa tta His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His Val Ile Lys Leu 105 110 115	392
agt cca gat gaa caa ggt gtg gat att ctt ata gtg ctc ata ttt cga Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val Leu Ile Phe Arg 120 125 130	440
tac cca tct act gat agt gct gaa caa atc aag aaa aaa att gaa aag Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys Lys Ile Glu Lys 135 140 145	488
gct tta tat caa agt ttg aag acc aaa caa ttg tct ttg acc ata aac Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser Leu Thr Ile Asn 150 155 160	536
aaa cca tca ttt aga ctc aca cct att gac agc aaa aag atg agg aat Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys Lys Met Arg Asn 165 170 175 180	584
ctt ctc aac agt cgc tgt gga ata agg atg aca tct tca aac atg cca Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser Ser Asn Met Pro 185 190 195	632
tta cca gca tcc tct act caa aga att gtc caa gga agg gaa aca Leu Pro Ala Ser Ser Thr Gln Arg Ile Val Gln Gly Arg Glu Thr 200 205 210	680
gct atg gaa ggg gaa tgg cca tgg cag gcc agc ctc cag ctc ata ggg Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Leu Ile Gly 215 220 225	728
tca ggc cat cag tgt gga gcc agc ctc atc agt aac aca tgg ctg ctc Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn Thr Trp Leu Leu 230 235 240	776
aca gca gct cac tgc ttt tgg aaa aat aaa gac cca act caa tgg att Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro Thr Gln Trp Ile 245 250 255 260	824
gct act ttt ggt gca act ata aca cca ccc gca gtg aaa cga aat gtg Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val Lys Arg Asn Val 265 270 275	872
agg aaa att att ctt cat gag aat tac cat aga gaa aca aat gaa aat	920

Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu Thr Asn Glu Asn			
280	285	290	
gac att gct ttg gtt cag ctc tct act gga gtt gag ttt tca aat ata			968
Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu Phe Ser Asn Ile			
295	300	305	
gtc cag aga gtt tgc ctc cca gac tca tct ata aag ttg cca cct aaa			1016
Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys Leu Pro Pro Lys			
310	315	320	
aca agt gtg ttc gtc aca gga ttt gga tcc att gta gat gat gga cct			1064
Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val Asp Asp Gly Pro			
325	330	335	340
ata caa aat aca ctt cgg caa gcc aga gtg gaa acc ata agc act gat			1112
Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr Ile Ser Thr Asp			
345	350	355	
gtg tgt aac aga aag gat gtg tat gat ggc ctg ata act cca gga atg			1160
Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile Thr Pro Gly Met			
360	365	370	
tta tgt gct gga ttc atg gaa gga aaa ata gat gca tgt aag gga gat			1208
Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala Cys Lys Gly Asp			
375	380	385	
tct ggt gga cct ctg gtt tat gat aat cat gac atc tgg tac att gta			1256
Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile Trp Tyr Ile Val			
390	395	400	
ggg ata gta agt tgg gga caa tca tgt gca ctt ccc aaa aaa cct gga			1304
Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro Lys Lys Pro Gly			
405	410	415	420
gtc tac acc aga gta act aag tat cga gat tgg att gcc tca aag act			1352
Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile Ala Ser Lys Thr			
425	430	435	
ggg atg tag tgtggattgt ccatgaggta tacacatggc acacagagct			1401
Gly Met *			
gataactcctg cgtatTTTgt attgtttaaa ttcatTTact ttggattAGT gcttttgcta			1461
gatgtcaaga agccCTTCAG acccagacAA atctaataTC ctgaggTggc cttacataAC			1521
gtaggaccaa acccTCTcta ccatgaggGA agaAGACACA gcaaatgaca gacAGCACCT			1581
atTCCTTact cacaAGGGAA actgCTTGTG atactTCCTA ataAGATAAA taagtggTTT			1641
CCCTCAATTG aagACAGGAA catcATTTC cacAGGAT GAAGAGCTGC cAGTAATGCC			1701
aaaATCTTAC cTCATATAAT acCTGGAGCA tGTGAGATT TTCTAGTGA AAGAAACAGT			1761
CTTCCCTGAA gACTCAGGGC TTCAACATC TAGAACTGAT AAGTGGACCT TCAGTGTGCA			1821
agaATGGAGA AGCATGGGAT TTGcATTATG ACTTGAACTG GGCTTATATC TAATAATACA			1881
gAGCAGTATC ACTAACCTCA ACAGTTGACA TTTAAAAGT TTTAAATGT ATCTGAACCT			1941
GCTGTTAACa CAGTGTATA ACTCAAGCAC TAGCTTCAGG AAGCATGTTG TGTGTTAACG			2001
aAGCTTTCT GATTtATTCT TAAACAGCAT CTGCGCATCT ATATGTTAGT AGCAGTTGGC			2061
CCAGAAAGGA CAAAAAAAGAA AAAAAGAAAGAA AAAAAGAAAGAA			2100

<210> 16
<211> 438
<212> PRT
<213> Homo sapien

<400> 16
 Met Met Tyr Thr Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala
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 Glu Tyr Gln Arg Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu
 20 25 30
 Phe Thr Leu Ala Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val
 35 40 45
 Thr His Phe Val Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser
 50 55 60
 Phe Lys Val Thr Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser
 65 70 75 80
 Ser Arg Glu Phe Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser
 85 90 95
 Arg Ile Phe Arg His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His
 100 105 110
 Val Ile Lys Leu Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val
 115 120 125
 Leu Ile Phe Arg Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys
 130 135 140
 Lys Ile Glu Lys Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser
 145 150 155 160
 Leu Thr Ile Asn Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys
 165 170 175
 Lys Met Arg Asn Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser
 180 185 190
 Ser Asn Met Pro Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln
 195 200 205
 Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
 210 215 220
 Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn
 225 230 235 240
 Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro
 245 250 255
 Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val
 260 265 270
 Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu
 275 280 285
 Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu
 290 295 300
 Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys
 305 310 315 320
 Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val
 325 330 335
 Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr
 340 345 350
 Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile
 355 360 365
 Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala
 370 375 380
 Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile
 385 390 395 400
 Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro
 405 410 415
 Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile
 420 425 430
 Ala Ser Lys Thr Gly Met
 435

<210> 17

<211> 702

<212> DNA

24745-1613

Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
 210 215 220

gat tgg att gcc tca aag act ggt atg tag
 Asp Trp Ile Ala Ser Lys Thr Gly Met *
 225 230

702

<210> 18
 <211> 233
 <212> PRT
 <213> Homo sapien

<400> 18
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 Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu
 20 25 30
 Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
 35 40 45
 Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
 50 55 60
 Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
 65 70 75 80
 His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr
 85 90 95
 Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser
 100 105 110
 Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly
 115 120 125
 Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg
 130 135 140
 Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp
 145 150 155 160
 GLy Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys
 165 170 175
 Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn
 180 185 190
 His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys
 195 200 205
 Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
 210 215 220
 Asp Trp Ile Ala Ser Lys Thr Gly Met
 225 230

<210> 19
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 19
 tctctcgaga aaagaattgt ccaaggaagg gaaacagcta tg

42

<210> 20
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Primer

<400> 20
agatgagtct gggaggctaa ctctctggac tat 33

<210> 21
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
attcgcggcc gcctacatac cagtcttga ggcaat 35

<210> 22
<211> 33
<212> DNA
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<220>
<223> Primer

<400> 22
atagtccaga gagtttagcct cccagactca tct 33